SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1

<130> D0073 CNT

<150> US 60/266,518
<151> 2001-02-05

<150> US 10/067,443
<151> 2002-02-05

<150> US 60/282,814
<151> 2001-04-10

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<170> PatentIn version 3.2

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gtttgcgccc gtcgccgcct tacagccgac aggagaccag cgctacccaa gtcacgtggg 180

ttcagcctgc agctttcttg gcccgaaagg gaattatcta tagagtaagt atg cta 236
Met Leu
1

atc ttg act aag act gca gga gtt ttt ttt aaa cca tca aaa agg aaa 284
Ile Leu Thr Lys Thr Ala Gly Val Phe Phe Lys Pro Ser Lys Arg Lys
5 10 15

gtt tat gaa ttt tta aga agt ttt aat ttt cat cct gga aca cta ttt 332
Val Tyr Glu Phe Leu Arg Ser Phe Asn Phe His Pro Gly Thr Leu Phe
20 25 30

ctt cat aaa ata gta ttg gga att gaa act agt tgt gat gat aca gca 380
Leu His Lys Ile Val Leu Gly Ile Glu Thr Ser Cys Asp Asp Thr Ala
35 40 45 50

gct gct gtg gtg gat gaa act gga aat gtg ttg gga gaa gca ata cat 428
Ala Ala Val Val Asp Glu Thr Gly Asn Val Leu Gly Glu Ala Ile His
55 60 65

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tcc caa act gaa gtt cat tta aaa aca ggt ggg att gtt cct cca gca      476
Ser Gln Thr Glu Val His Leu Lys Thr Gly Gly Ile Val Pro Pro Ala
            70                  75                  80

gct caa cag ctt cac aga gaa aat att caa cga ata gta caa gaa gct      524
Ala Gln Gln Leu His Arg Glu Asn Ile Gln Arg Ile Val Gln Glu Ala
        85                  90                  95

ctt tct gcc agt gga gtc tct cca agt gac ctc tca gca att gca act      572
Leu Ser Ala Ser Gly Val Ser Pro Ser Asp Leu Ser Ala Ile Ala Thr
    100                 105                 110

acc ata aaa cca gga ctt gct tta agc ctg gga gtg ggc tta tca ttt      620
Thr Ile Lys Pro Gly Leu Ala Leu Ser Leu Gly Val Gly Leu Ser Phe
115                 120                 125                 130

agc tta cag ctg gta gga cag tta aaa aag cca ttc att ccc att cat      668
Ser Leu Gln Leu Val Gly Gln Leu Lys Lys Pro Phe Ile Pro Ile His
                135                 140                 145

cat atg gag gct cat gca ctt act att agg ttg acc aat aaa gta gaa      716
His Met Glu Ala His Ala Leu Thr Ile Arg Leu Thr Asn Lys Val Glu
            150                 155                 160

ttt cct ttt tta gtt ctt ttg att tct gga ggt cac tgt ctg ttg gca      764
Phe Pro Phe Leu Val Leu Leu Ile Ser Gly Gly His Cys Leu Leu Ala
        165                 170                 175

tta gtt caa gga gtt tca gat ttt ctg ctt ctt gga aag tct ttg gac      812
Leu Val Gln Gly Val Ser Asp Phe Leu Leu Leu Gly Lys Ser Leu Asp
    180                 185                 190

ata gca cca ggt gac atg ctt gac aag gtg gca aga aga ctt tct tta      860
Ile Ala Pro Gly Asp Met Leu Asp Lys Val Ala Arg Arg Leu Ser Leu
195                 200                 205                 210

ata aaa cat cca gag tgc tcc acc atg agt ggt ggg aaa gcc ata gaa      908
Ile Lys His Pro Glu Cys Ser Thr Met Ser Gly Gly Lys Ala Ile Glu
                215                 220                 225

cat ttg gcc aaa caa gga aat aga ttt cat ttt gac atc aaa cct ccc      956
His Leu Ala Lys Gln Gly Asn Arg Phe His Phe Asp Ile Lys Pro Pro
            230                 235                 240

ttg cat cat gct aaa aat tgt gat ttt tct ttt act gga ctt caa cac     1004
Leu His His Ala Lys Asn Cys Asp Phe Ser Phe Thr Gly Leu Gln His
        245                 250                 255

gtt act gat aaa ata ata atg aaa aag gaa aaa gag gaa ggt att gag     1052
Val Thr Asp Lys Ile Ile Met Lys Lys Glu Lys Glu Glu Gly Ile Glu
    260                 265                 270

aag ggg caa atc ctg tct tca gca gca gac att gct gcc aca gta cag     1100
Lys Gly Gln Ile Leu Ser Ser Ala Ala Asp Ile Ala Ala Thr Val Gln
275                 280                 285                 290
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cac aca atg gca tgt cat ctt gtg aaa aga aca cat cgg gct att ctg     1148
His Thr Met Ala Cys His Leu Val Lys Arg Thr His Arg Ala Ile Leu
                295                 300                 305

ttt tgt aag cag aga gac ttg tta cct caa aat aat gca gta ctg gtt     1196
Phe Cys Lys Gln Arg Asp Leu Leu Pro Gln Asn Asn Ala Val Leu Val
            310                 315                 320

gca tct ggt ggt gtc gca agt aac ttc tat atc cgc aga gct ctg gaa     1244
Ala Ser Gly Gly Val Ala Ser Asn Phe Tyr Ile Arg Arg Ala Leu Glu
        325                 330                 335

att tta aca aac gca aca cag tgc act ttg ttg tgt cct cct ccc aga     1292
Ile Leu Thr Asn Ala Thr Gln Cys Thr Leu Leu Cys Pro Pro Pro Arg
    340                 345                 350

cta tgc act gat aat ggc att atg att gca tgg aat ggt att gaa aga     1340
Leu Cys Thr Asp Asn Gly Ile Met Ile Ala Trp Asn Gly Ile Glu Arg
355                 360                 365                 370

cta cgt gct ggc ttg ggc att tta cat gac ata gaa ggc atc cgc tat     1388
Leu Arg Ala Gly Leu Gly Ile Leu His Asp Ile Glu Gly Ile Arg Tyr
                375                 380                 385

gaa cca aaa tgt cct ctt gga gta gac ata tca aaa gaa gtt gga gaa     1436
Glu Pro Lys Cys Pro Leu Gly Val Asp Ile Ser Lys Glu Val Gly Glu
            390                 395                 400

gct tcc ata aaa gta cca caa tta aaa atg gag ata tgatttctgc          1482
Ala Ser Ile Lys Val Pro Gln Leu Lys Met Glu Ile
        405                 410

tgttcaaaaa agtccctaaa gggtctcact ctctgacctc agctggagta cagtagccag   1542

atcacaactc actgcaaccc tgacttcctg aactcaagaa atcctcctgc cttagcctct   1602

tgaatagccg ggactacagg tgtgcatgtc catgcccagc caactttatt tctatttttt   1662

gtagagacag gctcttgcca tgttgcccgg gctggtcctg aactgctgaa ttcaagtgat   1722

cctcccacct tggcctccag aagtgctggg attatgggtg tgagccacca tgcctagcca   1782

aaatgtttct taaggtatac attttgggtc ttagaagact tatacatttg taatatttat   1842

tactaaatat ctcaaagtat tacaataaat gttaccatgt gagctacttt gaatcaggct   1902

tcttgcacac caatttaaaa atgttaactc ttgatatata cactagttat accactcatg   1962

tcagtcaata aattttaagg tttaagtgca ggcctttgtt tacagaaatc ctaatttttt   2022

gaaaccataa ctctgacctg acactaaatt cctgtagaca tgctaaggaa aatctgctta   2082

gtatcgagat caagaacttc cattcaaaaa gattattcag ttatgttatt tgcatattac   2142

cattgttaaa aataaaaaaa tttttaaaag atgaaaaaaa aaaaaaaaaa aaaaa        2197
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<213> Homo sapiens

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Arg Lys Val Tyr Glu Phe Leu Arg Ser Phe Asn Phe His Pro Gly Thr
20 25 30

Leu Phe Leu His Lys Ile Val Leu Gly Ile Glu Thr Ser Cys Asp Asp
35 40 45

Thr Ala Ala Ala Val Val Asp Glu Thr Gly Asn Val Leu Gly Glu Ala
50 55 60

Ile His Ser Gln Thr Glu Val His Leu Lys Thr Gly Gly Ile Val Pro
65 70 75 80

Pro Ala Ala Gln Gln Leu His Arg Glu Asn Ile Gln Arg Ile Val Gln
85 90 95

Glu Ala Leu Ser Ala Ser Gly Val Ser Pro Ser Asp Leu Ser Ala Ile
100 105 110

Ala Thr Thr Ile Lys Pro Gly Leu Ala Leu Ser Leu Gly Val Gly Leu
115 120 125

Ser Phe Ser Leu Gln Leu Val Gly Gln Leu Lys Lys Pro Phe Ile Pro
130 135 140

Ile His His Met Glu Ala His Ala Leu Thr Ile Arg Leu Thr Asn Lys
145 150 155 160

Val Glu Phe Pro Phe Leu Val Leu Leu Ile Ser Gly Gly His Cys Leu
165 170 175

Leu Ala Leu Val Gln Gly Val Ser Asp Phe Leu Leu Leu Gly Lys Ser
180 185 190

Leu Asp Ile Ala Pro Gly Asp Met Leu Asp Lys Val Ala Arg Arg Leu
195 200 205

Ser Leu Ile Lys His Pro Glu Cys Ser Thr Met Ser Gly Gly Lys Ala
210 215 220

Ile Glu His Leu Ala Lys Gln Gly Asn Arg Phe His Phe Asp Ile Lys
225 230 235 240

Pro Pro Leu His His Ala Lys Asn Cys Asp Phe Ser Phe Thr Gly Leu
245 250 255

Gln His Val Thr Asp Lys Ile Ile Met Lys Lys Glu Lys Glu Glu Gly
260 265 270

Ile Glu Lys Gly Gln Ile Leu Ser Ser Ala Ala Asp Ile Ala Ala Thr
275 280 285

Val Gln His Thr Met Ala Cys His Leu Val Lys Arg Thr His Arg Ala
290 295 300

Ile Leu Phe Cys Lys Gln Arg Asp Leu Leu Pro Gln Asn Asn Ala Val
305 310 315 320

Leu Val Ala Ser Gly Gly Val Ala Ser Asn Phe Tyr Ile Arg Arg Ala
325 330 335

Leu Glu Ile Leu Thr Asn Ala Thr Gln Cys Thr Leu Leu Cys Pro Pro
340 345 350

Pro Arg Leu Cys Thr Asp Asn Gly Ile Met Ile Ala Trp Asn Gly Ile
355 360 365

Glu Arg Leu Arg Ala Gly Leu Gly Ile Leu His Asp Ile Glu Gly Ile
370 375 380

Arg Tyr Glu Pro Lys Cys Pro Leu Gly Val Asp Ile Ser Lys Glu Val
385 390 395 400

Gly Glu Ala Ser Ile Lys Val Pro Gln Leu Lys Met Glu Ile
405 410

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<213> Arabidopsis thaliana

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1 5 10 15

Leu Tyr Pro Gly Ile Ser Ile Leu Ala Arg Asn Asn Asn Ser Leu Arg
20 25 30

Leu Gln Lys His His Lys Leu Lys Thr Lys Thr Pro Thr Phe Ser Leu
35 40 45

Ile Ser Pro Ser Ser Ser Pro Asn Phe Gln Arg Thr Arg Phe Tyr Ser
50 55 60

Thr Glu Thr Arg Ile Ser Ser Leu Pro Tyr Ser Glu Asn Pro Asn Phe
65 70 75 80

Asp Asp Asn Leu Val Val Leu Gly Ile Glu Thr Ser Cys Asp Asp Thr
85 90 95

Ala Ala Ala Val Val Ser Pro Phe Asn His Leu Ser Ser Ser Cys Arg
100 105 110

Ala Glu Leu Leu Val Gln Tyr Gly Gly Val Ala Pro Lys Gln Ala Glu
115 120 125

Glu Ala His Ser Arg Val Ile Asp Lys Val Val Gln Asp Ala Leu Asp
130 135 140

Lys Ala Asn Leu Thr Glu Lys Asp Leu Ser Ala Val Ala Val Thr Ile
145 150 155 160

Gly Pro Gly Leu Ser Leu Cys Leu Arg Val Gly Val Arg Lys Ala Arg
165 170 175

Arg Val Ala Gly Asn Phe Ser Leu Pro Ile Val Gly Val His His Met
180 185 190

Glu Ala His Ala Leu Val Ala Arg Leu Val Glu Gln Glu Leu Ser Phe
195 200 205

Pro Phe Met Ala Leu Leu Ile Ser Gly Gly His Asn Leu Leu Val Leu

```
    210                 215                 220

Ala His Lys Leu Gly Gln Tyr Thr Gln Leu Gly Thr Thr Val Asp Asp
225                 230                 235                 240

Ala Ile Gly Glu Ala Phe Asp Lys Thr Ala Lys Trp Leu Gly Leu Asp
                245                 250                 255

Met His Arg Ser Gly Gly Pro Ala Val Glu Glu Leu Ala Leu Glu Gly
            260                 265                 270

Asp Ala Lys Ser Val Lys Phe Asn Val Pro Met Lys Tyr His Lys Asp
        275                 280                 285

Cys Asn Phe Ser Tyr Ala Gly Leu Lys Thr Gln Val Arg Leu Ala Ile
    290                 295                 300

Glu Ala Lys Glu Ile Arg Asn Arg Ala Asp Ile Ala Ala Ser Phe Gln
305                 310                 315                 320

Arg Val Ala Val Leu His Leu Glu Glu Lys Cys Glu Arg Ala Ile Asp
                325                 330                 335

Trp Ala Leu Glu Leu Glu Pro Ser Ile Lys His Met Val Ile Ser Gly
            340                 345                 350

Gly Val Ala Ser Asn Lys Tyr Val Arg Leu Arg Leu Asn Asn Ile Val
        355                 360                 365

Glu Asn Lys Asn Leu Lys Leu Val Cys Pro Pro Pro Ser Leu Cys Thr
    370                 375                 380

Asp Asn Gly Val Met Val Ala Trp Thr Gly Leu Glu His Phe Arg Val
385                 390                 395                 400

Gly Arg Tyr Asp Pro Pro Pro Pro Ala Thr Glu Pro Glu Asp Tyr Val
                405                 410                 415

Tyr Asp Leu Arg Pro Arg Trp Pro Leu Gly Glu Glu Tyr Ala Lys Gly
            420                 425                 430

Arg Ser Glu Ala Arg Ser Met Arg Thr Ala Arg Ile His Pro Ser Leu
        435                 440                 445
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Thr Ser Ile Ile Arg Ala Asp Ser Leu Gln Gln Gln Thr Gln Thr
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<213> Caenorhabditis elegans

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Phe Cys Arg Asn Tyr Ser Val Lys Val Leu Gly Ile Glu Thr Ser Cys
20 25 30

Asp Asp Thr Ala Val Ala Ile Val Asn Glu Lys Arg Glu Ile Leu Ser
35 40 45

Ser Glu Arg Tyr Thr Glu Arg Ala Ile Gln Arg Gln Gln Gly Gly Ile
50 55 60

Asn Pro Ser Val Cys Ala Leu Gln His Arg Glu Asn Leu Pro Arg Leu
65 70 75 80

Ile Glu Lys Cys Leu Asn Asp Ala Gly Thr Ser Pro Lys Asp Leu Asp
85 90 95

Ala Val Ala Val Thr Val Thr Pro Gly Leu Val Ile Ala Leu Lys Glu
100 105 110

Gly Ile Ser Ala Ala Ile Gly Phe Ala Lys Lys His Arg Leu Pro Leu
115 120 125

Ile Pro Val His His Met Arg Ala His Ala Leu Ser Ile Leu Leu Val
130 135 140

Asp Asp Ser Val Arg Phe Pro Phe Ser Ala Val Leu Leu Ser Gly Gly
145 150 155 160

His Ala Leu Ile Ser Val Ala Glu Asp Val Glu Lys Phe Lys Leu Tyr
165 170 175

Gly Gln Ser Val Ser Gly Ser Pro Gly Glu Cys Ile Asp Lys Val Ala
180 185 190

Arg Gln Leu Gly Asp Leu Gly Ser Glu Phe Asp Gly Ile His Val Gly
195 200 205

Ala Ala Val Glu Ile Leu Ala Ser Arg Ala Ser Ala Asp Gly His Leu
210 215 220

Arg Tyr Pro Ile Phe Leu Pro Asn Val Pro Lys Ala Asn Met Asn Phe
225 230 235 240

Asp Gln Ile Lys Gly Ser Tyr Leu Asn Leu Leu Glu Arg Leu Arg Lys
245 250 255

Asn Ser Glu Thr Ser Ile Asp Ile Pro Asp Phe Cys Ala Ser Leu Gln
260 265 270

Asn Thr Val Ala Arg His Ile Ser Ser Lys Leu His Ile Phe Phe Glu
275 280 285

Ser Leu Ser Glu Gln Glu Lys Leu Pro Lys Gln Leu Val Ile Gly Gly
290 295 300

Gly Val Ala Ala Asn Gln Tyr Ile Phe Gly Ala Ile Ser Lys Leu Ser
305 310 315 320

Ala Ala His Asn Val Thr Thr Ile Lys Val Leu Leu Ser Leu Cys Thr
325 330 335

Asp Asn Ala Glu Met Ile Ala Tyr Ser Gly Leu Leu Met Leu Val Asn
340 345 350

Arg Ser Glu Ala Ile Trp Trp Arg Pro Asn Asp Ile Pro Asp Thr Ile
355 360 365

Tyr Ala His Ala Arg Ser Asp Ile Gly Thr Asp Ala Ser Ser Glu Ile
370 375 380

Ile Asp Thr Pro Arg Arg Lys Leu Val Thr Ser Thr Ile His Gly Thr
385 390 395 400

Glu Arg Ile Arg Phe Arg Asn Leu Asp Asp Phe Lys Lys Pro Lys Ser

405 410 415

Pro Lys Thr Thr Glu
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<211> 327
<212> PRT
<213> Thermotoga maritima

<400> 5

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1 5 10 15

Val Leu Asp Asp Gly Lys Asn Val Val Val Asn Phe Thr Val Ser Gln
20 25 30

Ile Glu Val His Gln Lys Phe Gly Gly Val Val Pro Glu Val Ala Ala
35 40 45

Arg His His Leu Lys Asn Leu Pro Ile Leu Leu Lys Lys Ala Phe Glu
50 55 60

Lys Val Pro Pro Glu Thr Val Asp Val Val Ala Ala Thr Tyr Gly Pro
65 70 75 80

Gly Leu Ile Gly Ala Leu Leu Val Gly Leu Ser Ala Ala Lys Gly Leu
85 90 95

Ala Ile Ser Leu Glu Lys Pro Phe Val Gly Val Asn His Val Glu Ala
100 105 110

His Val Gln Ala Val Phe Leu Ala Asn Pro Asp Leu Lys Pro Pro Leu
115 120 125

Val Val Leu Met Val Ser Gly Gly His Thr Gln Leu Met Lys Val Asp
130 135 140

Glu Asp Tyr Ser Met Glu Val Leu Gly Glu Thr Leu Asp Asp Ser Ala
145 150 155 160

Gly Glu Ala Phe Asp Lys Val Ala Arg Leu Leu Gly Leu Gly Tyr Pro
165 170 175

Gly Gly Pro Val Ile Asp Arg Val Ala Lys Lys Gly Asp Pro Glu Lys
180 185 190

Tyr Ser Phe Pro Arg Pro Met Leu Asp Asp Asp Ser Tyr Asn Phe Ser
195 200 205

Phe Ala Gly Leu Lys Thr Ser Val Leu Tyr Phe Leu Gln Arg Glu Lys
210 215 220

Gly Tyr Lys Val Glu Asp Val Ala Ala Ser Phe Gln Lys Ala Val Val
225 230 235 240

Asp Ile Leu Val Glu Lys Thr Phe Arg Leu Ala Arg Asn Leu Gly Ile
245 250 255

Arg Lys Ile Ala Phe Val Gly Gly Val Ala Ala Asn Ser Met Leu Arg
260 265 270

Glu Glu Val Arg Lys Arg Ala Glu Arg Trp Asn Tyr Glu Val Phe Phe
275 280 285

Pro Pro Leu Glu Leu Cys Thr Asp Asn Ala Leu Met Val Ala Lys Ala
290 295 300

Gly Tyr Glu Lys Ala Lys Arg Gly Met Phe Ser Pro Leu Ser Leu Asn
305 310 315 320

Ala Asp Pro Asn Leu Asn Val
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<213> Helicobacter pylori

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Met Ile Leu Ser Ile Glu Ser Ser Cys Asp Asp Ser Ser Leu Ala Leu
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Thr Arg Ile Glu Asp Ala Gln Leu Ile Ala His Phe Lys Ile Ser Gln
20 25 30

Glu Lys His His Ser Ser Tyr Gly Gly Val Val Pro Glu Leu Ala Ser

```
        35                  40                  45

Arg Leu His Ala Glu Asn Leu Pro Leu Leu Leu Glu Arg Ile Lys Ile
    50                  55                  60

Ser Leu Asn Lys Asp Phe Ser Lys Ile Lys Ala Ile Ala Ile Thr Asn
65                  70                  75                  80

Gln Pro Gly Leu Ser Val Thr Leu Ile Glu Gly Leu Met Met Ala Lys
                85                  90                  95

Ala Leu Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Glu Asp His Leu
            100                 105                 110

Arg Gly His Val Tyr Ser Leu Phe Ile Asn Glu Lys Gln Thr Cys Met
        115                 120                 125

Pro Leu Ser Val Leu Leu Val Ser Gly Gly His Ser Leu Ile Leu Glu
    130                 135                 140

Ala Arg Asp Tyr Glu Asn Ile Lys Ile Val Ala Thr Ser Leu Asp Asp
145                 150                 155                 160

Ser Phe Gly Glu Ser Phe Asp Lys Val Ser Lys Met Leu Asp Leu Gly
                165                 170                 175

Tyr Pro Gly Gly Pro Ile Val Glu Lys Leu Ala Leu Asp Tyr Arg His
            180                 185                 190

Pro Asn Glu Pro Leu Met Phe Pro Ile Pro Leu Lys Asn Ser Pro Asn
        195                 200                 205

Leu Ala Phe Ser Phe Ser Gly Leu Lys Asn Ala Val Arg Leu Glu Val
    210                 215                 220

Glu Lys Asn Ala Pro Asn Leu Asn Glu Ala Ile Lys Gln Lys Ile Gly
225                 230                 235                 240

Tyr His Phe Gln Ser Ala Ala Ile Glu His Leu Ile Gln Gln Thr Lys
                245                 250                 255

Arg Tyr Phe Lys Ile Lys Arg Pro Lys Ile Phe Gly Ile Val Gly Gly
            260                 265                 270
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Ala Ser Gln Asn Leu Ala Leu Arg Lys Ala Phe Glu Asn Leu Cys Asp
        275                 280                 285

Ala Phe Asp Cys Lys Leu Val Leu Ala Pro Leu Glu Phe Cys Ser Asp
    290                 295                 300

Asn Ala Ala Met Ile Gly Arg Ser Ser Leu Glu Ala Tyr Gln Lys Lys
305                 310                 315                 320

Arg Phe Val Pro Leu Glu Lys Ala Asn Ile Ser Pro Arg Thr Leu Leu
                325                 330                 335

Lys Ser Phe Glu
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<213> Homo sapiens

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Leu Glu Ile Leu Thr Asn Ala Thr Gln Cys Thr Leu Leu Cys
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Val Phe Phe Lys Pro Ser Lys Arg Lys Val Tyr Glu Phe
1               5                   10
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<210> 9
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<213> Homo sapiens

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Glu Ala His Ala Leu Thr Ile Arg Leu Thr Asn Lys Val
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<210> 11
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Leu Thr Ile Arg Leu Thr Asn Lys Val Glu Phe Pro Phe
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Gly Leu Gln His Val Thr Asp Lys Ile Ile Met Lys Lys
1 5 10

<210> 13
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<212> PRT
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<400> 13

His Leu Val Lys Arg Thr His Arg Ala Ile Leu Phe Cys
1 5 10

<210> 14
<211> 13
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<213> Homo sapiens

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Glu Val Gly Glu Ala Ser Ile Lys Val Pro Gln Leu Lys
1 5 10

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<212> DNA
<213> artificial

<220>
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tcttgtacta ttcgttgaat 80

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<211> 20
<212> DNA
<213> homo sapiens

<400> 16
ctgctgtggt ggatgaaact 20

<210> 17
<211> 20
<212> DNA
<213> homo sapiens

<400> 17
tgcatgagcc tccatatgat 20

<210> 18
<211> 162
<212> PRT
<213> homo sapiens

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Met Arg Ile Leu Val Leu Gly Val Gly Asn Ile Leu Leu Thr Asp Glu
1 5 10 15

Ala Ile Gly Val Arg Ile Val Glu Ala Leu Glu Gln Arg Tyr Ile Leu
20 25 30

Pro Asp Tyr Val Glu Ile Leu Asp Gly Gly Thr Ala Gly Met Glu Leu
35 40 45

Leu Gly Asp Met Ala Asn Arg Asp His Leu Ile Ile Ala Asp Ala Ile
50 55 60

Val Ser Lys Lys Asn Ala Pro Gly Thr Met Met Ile Leu Arg Asp Glu
65 70 75 80

Glu Val Pro Ala Leu Phe Thr Asn Lys Ile Ser Pro His Gln Leu Gly
85 90 95

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Leu Ala Asp Val Leu Ser Ala Leu Arg Phe Thr Gly Glu Phe Pro Lys
            100                 105                 110

Lys Leu Thr Leu Val Gly Val Ile Pro Glu Ser Leu Glu Pro His Ile
        115                 120                 125

Gly Leu Thr Pro Thr Val Glu Ala Met Ile Glu Pro Ala Leu Glu Gln
    130                 135                 140

Val Leu Ala Ala Leu Arg Glu Ser Gly Val Glu Ala Ile Pro Arg Ser
145                 150                 155                 160

Asp Ser
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<210> 19
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<212> PRT
<213> homo sapiens

<400> 19

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Met Leu Ile Leu Thr Lys Thr Ala Gly Val Phe Phe Lys Pro Ser Lys
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Arg Lys Val Tyr Glu Phe Leu Arg Ser Phe Asn Phe His Pro Glu Thr
            20                  25                  30

Leu Phe Leu His Lys Ile Val Leu Gly Ile Glu Thr Ser Cys Asp Asp
        35                  40                  45

Thr Ala Ala Ala Val Val Asp Glu Thr Gly Asn Val Leu Gly Glu Ala
    50                  55                  60

Ile His Ser Gln Thr Glu Val His Leu Lys Thr Gly Gly Ile Val Pro
65                  70                  75                  80

Pro Ala Ala Gln Gln Leu His Arg Glu Asn Ile Gln Arg Ile Val Gln
                85                  90                  95

Glu Ala Leu Ser Ala Ser Gly Val Ser Pro Ser Asp Leu Ser Ala Ile
            100                 105                 110
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Ala Thr Thr Ile Lys Pro Gly Leu Ala Leu Ser Leu Gly Val Gly Leu
115 120 125

Ser Phe Ser Leu Gln Leu Val Gly Gln Leu Lys Lys Pro Phe Ile Pro
130 135 140

Ile His His Met Glu Ala His Ala Leu Thr Ile Arg Leu Thr Asn Lys
145 150 155 160

Val Glu Phe Pro Phe Leu Val Leu Leu Ile Ser Gly Gly His Cys Leu
165 170 175

Leu Ala Leu Val Gln Gly Val Ser Asp Phe Leu Leu Leu Gly Lys Ser
180 185 190

Leu Asp Ile Ala Pro Gly Asp Met Leu Asp Lys Val Ala Arg Arg Leu
195 200 205

Ser Leu Ile Lys His Pro Glu Cys Ser Thr Met Ser Gly Gly Lys Ala
210 215 220

Ile Glu His Leu Ala Lys Gln Gly Asn Arg Phe His Phe Asp Ile Lys
225 230 235 240

Pro Pro Leu His His Ala Lys Asn Cys Asp Phe Ser Phe Thr Gly Leu
245 250 255

Gln His Val Thr Asp Lys Ile Ile Met Lys Lys Glu Lys Glu Glu Gly
260 265 270

Ile Phe Leu Ile Ser Lys Val Glu Gln Ile Asn Ile Pro Gly Leu Cys
275 280 285

Leu Lys Ile Ala Ala His Phe Cys Arg Tyr Glu Lys Gly Gln Ile Leu
290 295 300

Ser Ser Ala Ala Asp Ile Ala Ala Thr Val Gln His Thr Met Ala Cys
305 310 315 320

His Leu Val Lys Arg Thr His Arg Ala Ile Leu Phe Cys Lys Gln Arg
325 330 335

Asp Leu Leu Pro Gln Asn Asn Ala Val Leu Val Ala Ser Gly Gly Val

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            340                 345                 350

Ala Ser Asn Phe Tyr Ile Arg Arg Ala Leu Glu Ile Leu Thr Asn Ala
        355                 360                 365

Thr Gln Cys Thr Leu Leu Cys Pro Pro Pro Arg Leu Cys Thr Asp Asn
    370                 375                 380

Gly Ile Met Ile Ala Trp Asn Gly Ile Glu Arg Leu Arg Gly Gly Leu
385                 390                 395                 400

Gly Ile Leu His Asp Ile Glu Gly Ile Arg Tyr Glu Pro Lys Cys Pro
                405                 410                 415

Leu Gly Val Asp Ile Ser Lys Glu Val Gly Glu Ala Ser Ile Lys Val
            420                 425                 430

Pro Gln Leu Lys Met Glu Ile
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<212> DNA
<213> homo sapiens

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cacattggcc aggctggtct cgaactccag gcctcaagtg atccacccac ctcggcctcc 14280

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tatttcttca taaaatagta ttgggaattg aaactagttg tgatgataca gcagctgctg 180

tggtggatga aactggaaat gtgttgggag aagcaataca ttcccaaact gaagttcatt 240

taaaaacagg tgggattgtt cctccagcag ctcaacagct tcacagagaa aatattcaac 300

gaatagtaca agaagctctt tctgccagtg gagtctctcc aagtgacctc tcagcaattg 360

caactaccat aaaaccagga cttgctttaa gcctgggagt gggcttatca tttagcttac 420

agctggtagg acagttaaaa aagccattca ttcccattca tcatatggag gctcatgcac 480

ttactattag gttgaccaat aaagtagaat ttccttttt agttcttttg atttctggag 540

gtcactgtct gttggcatta gttcaaggag tttcagattt tctgcttctt ggaaagtctt 600

tggacatagc accaggtgac atgcttgaca aggtggcaag aagactttct ttaataaaac 660

atccagagtg ctccaccatg agtggtggga aagccataga gcatttggcc aaacaaggaa 720

atagatttca ttttgacatc aaacctccct tgcatcatgc taaaaattgt gatttttctt 780

ttactggact tcaacacgtt actgataaaa taataatgaa aaaggaaaaa gaggaaggta 840

tatttctaat tagtaaagtt gaacagataa atattcctgg attgtgccta aaaatagctg 900

ctcatttctg caggtatgag aaggggcaaa tcctgtcttc agcagcagac attgctgcca 960

cagtacagca cacaatggca tgtcatcttg tgaaaagaac acatcgggct attctgtttt 1020

gtaagcagag agacttgtta cctcaaaata atgcagtact ggttgcatct ggtggtgtcg 1080

caagtaactt ctatatccgc agagctctgg aaattttaac aaacgcaaca cagtgcactt 1140

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ttgaaagact acgtggtggc ttgggcattt tacatgacat agaaggcatc cgctatgaac 1260

caaaatgtcc tcttggagta gacatatcaa aagaagttgg agaagcttcc ataaaagtac 1320

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Val Gln Gly Val Ser Asp Phe Leu Leu Leu Gly Lys Ser Leu Asp Ile
35 40 45

Ala Pro Gly Asp Met Leu Asp Lys Val Ala Arg Arg Leu Ser Leu Ile
50 55 60

Lys His Pro Glu Cys Ser Thr Met Ser Gly Gly Lys Ala Ile Glu His
65 70 75 80

Leu Ala Lys Gln Gly Asn Arg Phe His Phe Asp Ile Lys Pro Pro Leu
85 90 95

His His Ala Lys Asn Cys Asp Phe Ser Phe Thr Gly Leu Gln His Val
100 105 110

Thr Asp Lys Ile Ile Met Lys Lys Glu Lys Glu Glu Gly Ile Glu Lys
115 120 125

Gly Gln Ile Leu Ser Ser Ala Ala Asp Ile Ala Ala Thr Val Gln His
130 135 140

Thr Met Ala Cys His Leu Val Lys Arg Thr His Arg Ala Ile Leu Phe
145 150 155 160

Cys Lys Gln Arg Asp Leu Leu Pro Gln Asn Asn Ala Val Leu Val Ala
165 170 175

Ser Gly Gly Val Ala Ser Asn Phe Tyr Ile Arg Arg Ala Leu Glu Ile
180 185 190

Leu Thr Asn Ala Thr Gln Cys Thr Leu Leu Cys Pro Pro Pro Arg Leu
195 200 205

Cys Thr Asp Asn Gly Ile Met Ile Ala Trp Asn Gly Ile Glu Arg Leu
210 215 220

Arg Ala Gly Leu Gly Ile Leu His Asp Ile Glu Gly Ile Arg Tyr Glu
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Pro Lys Cys Pro Leu Gly Val Asp Ile Ser Lys Glu Val Gly Glu Ala
245 250 255

Ser Ile Lys Val Pro Gln Leu Lys Met Glu Ile
260 265

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cttcttggaa agtctttgga catagcacca ggtgacatgc ttgacaaggt ggcaagaaga 180

ctttctttaa taaaacatcc agagtgctcc accatgagtg gtgggaaagc catagaacat 240

ttggccaaac aaggaaatag atttcatttt gacatcaaac ctcccttgca tcatgctaaa 300

aattgtgatt tttcttttac tggacttcaa cacgttactg ataaaataat aatgaaaaag 360

gaaaaagagg aaggtattga gaaggggcaa atcctgtctt cagcagcaga cattgctgcc 420

acagtacagc acacaatggc atgtcatctt gtgaaaagaa cacatcgggc tattctgttt 480

tgtaagcaga gagacttgtt acctcaaaat aatgcagtac tggttgcatc tggtggtgtc 540

gcaagtaact tctatatccg cagagctctg gaaattttaa caaacgcaac acagtgcact 600

ttgttgtgtc ctcctcccag actatgcact gataatggca ttatgattgc atggaatggt 660

attgaaagac tacgtgctgg cttgggcatt ttacatgaca tagaaggcat ccgctatgaa 720

ccaaaatgtc ctcttggagt agacatatca aaagaagttg gagaagcttc cataaaagta 780

ccacaattaa aaatggagat atgatttctg ctgttcaaaa aagtccctaa agggtctcac 840

tctctgacct cagctggagt acagtagcca gatcacaact cactgcaacc ctgacttcct 900

gaactcaaga aatcctcctg ccttagcctc ttgaatagcc gggactacag gtgtgcatgt 960

ccatgcccag ccaactttat ttctattttt tgtagagaca ggctcttgcc atgttgcccg 1020

ggctggtcct gaactgctga attcaagtga tcctcccacc ttggcctcca gaagtgctgg 1080

gattatgggt gtgagccacc atgcctagcc aaaatgtttc ttaaggtata cattttgggt 1140

cttagaagac ttatacattt gtaatattta ttactaaata tctcaaagta ttacaataaa 1200

tgttaccatg tgagctactt tgaatcaggc ttcttgcaca ccaatttaaa aatgttaact 1260

cttgatatat acactagtta taccactcat gtcagtcaat aaattttaag gtttaagtgc 1320

aggcctttgt ttacagaaat cctaattttt tgaaaccata actctgacct gacactaaat 1380

tcctgtagac atgctaagga aaatctgctt agtatcgaga tcaagaactt ccattcaaaa 1440

agattattca gttatgttat ttgcatatta ccattgttaa aaataaaaaa atttttaaaa 1500

gatgaaaaaa aaaaaaaaaa aaaaaa 1526

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<400> 24

His His Met Glu Ala His
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<210> 25
<211> 179
<212> PRT
<213> homo sapiens

<400> 25

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Val Asp Glu Thr Gly Asn Val Leu Gly Glu Ala Ile His Ser Gln Thr
20 25 30

Glu Val His Leu Lys Thr Gly Gly Ile Val Pro Pro Ala Ala Gln Gln
35 40 45

Leu His Arg Glu Asn Ile Gln Arg Ile Val Gln Glu Ala Leu Ser Ala
50 55 60

Ser Gly Val Ser Pro Ser Asp Leu Ser Ala Ile Ala Thr Thr Ile Lys
65 70 75 80

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Pro Gly Leu Ala Leu Ser Leu Gly Val Gly Leu Ser Phe Ser Leu Gln
                85                  90                  95

Leu Val Gly Gln Leu Lys Lys Pro Phe Ile Pro Cys Cys Ala Thr Thr
            100                 105                 110

Cys Ala Thr Cys Ala Thr Ala Thr Gly Gly Ala Gly Gly Cys Thr Cys
        115                 120                 125

Ala Thr Gly Cys Ala Cys Thr Thr Ala Cys Thr Ala Thr Thr Ala Gly
    130                 135                 140

Gly Thr Thr Gly Ala Cys Cys Ala Ala Thr Ala Ala Ala Gly Thr Ala
145                 150                 155                 160

Gly Ala Ala Thr Thr Thr Cys Ile His His Met Glu Ala His Ala Leu
                165                 170                 175

Thr Ile Arg
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<210> 26
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Asp Tyr Lys Asp Asp Asp Asp Lys
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tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg    180

tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg    240

aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact    300

ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg    360
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agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420

catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480

atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540

ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg 600

acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660

acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720

gactctagag gat 733

<210> 28
<211> 421
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<400> 28

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Phe Cys Arg Asn Tyr Ser Val Lys Val Leu Gly Ile Glu Thr Ser Cys
20 25 30

Asp Asp Thr Ala Val Ala Ile Val Asn Glu Lys Arg Glu Ile Leu Ser
35 40 45

Ser Glu Arg Tyr Thr Glu Arg Ala Ile Gln Arg Gln Gln Gly Gly Ile
50 55 60

Asn Pro Ser Val Cys Ala Leu Gln His Arg Glu Asn Leu Pro Arg Leu
65 70 75 80

Ile Glu Lys Cys Leu Asn Asp Ala Gly Thr Ser Pro Lys Asp Leu Asp
85 90 95

Ala Val Ala Val Thr Val Thr Pro Gly Leu Val Ile Ala Leu Lys Glu
100 105 110

Gly Ile Ser Ala Ala Ile Gly Phe Ala Lys Lys His Arg Leu Pro Leu
115 120 125

Ile Pro Val His His Met Arg Ala His Ala Leu Ser Ile Leu Leu Val
130 135 140

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Asp Asp Ser Val Arg Phe Pro Phe Ser Ala Val Leu Leu Ser Gly Gly
145                 150                 155                 160

His Ala Leu Ile Ser Val Ala Glu Asp Val Glu Lys Phe Lys Leu Tyr
                165                 170                 175

Gly Gln Ser Val Ser Gly Ser Pro Gly Glu Cys Ile Asp Lys Val Ala
            180                 185                 190

Arg Gln Leu Gly Asp Leu Gly Ser Glu Phe Asp Gly Ile His Val Gly
        195                 200                 205

Ala Ala Val Glu Ile Leu Ala Ser Arg Ala Ser Ala Asp Gly His Leu
    210                 215                 220

Arg Tyr Pro Ile Phe Leu Pro Asn Val Pro Lys Ala Asn Met Asn Phe
225                 230                 235                 240

Asp Gln Ile Lys Gly Ser Tyr Leu Asn Leu Leu Glu Arg Leu Arg Lys
                245                 250                 255

Asn Ser Glu Thr Ser Ile Asp Ile Pro Asp Phe Cys Ala Ser Leu Gln
            260                 265                 270

Asn Thr Val Ala Arg His Ile Ser Ser Lys Leu His Ile Phe Phe Glu
        275                 280                 285

Ser Leu Ser Glu Gln Glu Lys Leu Pro Lys Gln Leu Val Ile Gly Gly
    290                 295                 300

Gly Val Ala Ala Asn Gln Tyr Ile Phe Gly Ala Ile Ser Lys Leu Ser
305                 310                 315                 320

Ala Ala His Asn Val Thr Thr Ile Lys Val Leu Leu Ser Leu Cys Thr
                325                 330                 335

Asp Asn Ala Glu Met Ile Ala Tyr Ser Gly Leu Leu Met Leu Val Asn
            340                 345                 350

Arg Ser Glu Ala Ile Trp Trp Arg Pro Asn Asp Ile Pro Asp Thr Ile
        355                 360                 365
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Tyr Ala His Ala Arg Ser Asp Ile Gly Thr Asp Ala Ser Ser Glu Ile
370 375 380

Ile Asp Thr Pro Arg Arg Lys Leu Val Thr Ser Thr Ile His Gly Thr
385 390 395 400

Glu Arg Ile Arg Phe Arg Asn Leu Asp Asp Phe Lys Lys Pro Lys Ser
405 410 415

Pro Lys Thr Thr Glu
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<210> 70
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<210> 71
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